RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _09/587,111A_

Source: _1FW16_

Date Processed by STIC: _12/21/04_

ENTERED

RAW SEQUENCE LISTING   DATE: 12/21/2004
PATENT APPLICATION: US/09/587,111A   TIME: 11:05:58

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\12212004\I587111A.raw

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 4 <110> APPLICANT: Millennium Pharmaceuticals, Inc.
 5        Curtis, Rory A.J.
 7 <120> TITLE OF INVENTION: NOVEL MEMBERS OF THE CAPSAICIN/VANILLOID
 8        RECEPTOR FAMILY OF PROTEINS AND USES THEREOF
11 <130> FILE REFERENCE: MPI98-093P2RCP3DV1AM
13 <140> CURRENT APPLICATION NUMBER: US 09/587,111A
14 <141> CURRENT FILING DATE: 2000-06-02
16 <150> PRIOR APPLICATION NUMBER: US 09/439,165
17 <151> PRIOR FILING DATE: 1999-11-12
19 <150> PRIOR APPLICATION NUMBER: US 09/421,134
20 <151> PRIOR FILING DATE: 1999-10-19
22 <150> PRIOR APPLICATION NUMBER: US 09/258,633
23 <151> PRIOR FILING DATE: 1999-02-26
25 <150> PRIOR APPLICATION NUMBER: US 60/114,078
26 <151> PRIOR FILING DATE: 1998-12-28
28 <150> PRIOR APPLICATION NUMBER: US 60/108,322
29 <151> PRIOR FILING DATE: 1998-11-13
31 <160> NUMBER OF SEQ ID NOS: 23
33 <170> SOFTWARE: FastSEQ for Windows Version 4.0
35 <210> SEQ ID NO: 1
36 <211> LENGTH: 3909
37 <212> TYPE: DNA
38 <213> ORGANISM: Homo Sapiens
40 <220> FEATURE:
41 <221> NAME/KEY: CDS
42 <222> LOCATION: (1113)...(3629)
44 <400> SEQUENCE: 1
45 gtgagcgcaa cgcactgcgg gcagtgagcg caacgcactg cgggcagtga gcgcaacgca 60
46 ctgcgggcag tgagcgcaac gcactgcggg cagtgagcgc aacgcactgc gggcagtgag 120
47 cgcaacgcac tgcgggcagt gagcgcaacg cactgcgggc agtgagcgca acgcacttgc 180
48 gggcagtgag cgcaacgcac tgcgggcagt gagcgcaacg cactgcgggc agtgagcgca 240
49 acgcactgcg ggcagtgagc gcaacgcact gcgggcagtg agcgcaacgc actgcgggca 300
50 gtgagcgcaa cgcactgcgg gcagtgagcg caacgcactg cgggcagtga gcgcaacgca 360
51 ctgcgggcag tgagcgcaac gcactgcggg cagtgagcgc aacgcactgc gggcagtgag 420
52 cgcaacgcac ttaatgtgag ttagctcact cattaggcac cccaggcttt acactttatg 480
53 cttccggctc gtatgttgtg tggaattgtg agcggataac aatttcacac aggaaacagc 540
54 tatgaccatg attacgccaa gctctaatac gactcactat agggaaagct ggtacgcctg 600
55 caggtaccgg tccggaattc ccgggtcgac ccacgcgtcc gaaaacacac ctctctgctg 660
56 tgggaagact gtgcaatggc acagccgcag agcttggttt gggaggttga agtgctctgg 720
57 ggagaattcg tagatcatcc tcagaaaagc cttgccctgg tgttctacca gaaaaacgtc 780
58 tcccaatcac ccagaaaagc tgtccacagt agtcccccct tatccacggg tgtcactttc 840
59 catgggttca gttatttgcg gtcaaccacg gtctgccaat attaaatgga aaattcttca 900
60 aacagttccc aagttttccc ttgtgcattg ttctgagcag tgtgatgaag agtctctgcc 960
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61 gtgccatctg ggatgcaaac cgtccctgtg tcccccacgt ccaggccgta gatgctcccc 1020
62 gccggtcagt cacttagtcg tcagatcgcc cgtcctggta tcacagtgct tctgttcagg 1080
63 ttgcacactg ggccacagag gatccagcaa gg atg aag aaa tgg agc agc aca 1133
64                                     Met Lys Lys Trp Ser Ser Thr
65                                      1                   5
67 gac ttg ggg aca gct gcg gac cca ctc caa aag gac acc tgc cca gac 1181
68 Asp Leu Gly Thr Ala Ala Asp Pro Leu Gln Lys Asp Thr Cys Pro Asp
69         10                  15                  20
71 ccc ctg gat gga gac cct aac tcc agg cca cct cca gcc aag ccc cag 1229
72 Pro Leu Asp Gly Asp Pro Asn Ser Arg Pro Pro Pro Ala Lys Pro Gln
73         25                  30                  35
75 ctc ccc acg gcc aag agc cgc acc cgg ctc ttt ggg aag ggt gac tcg 1277
76 Leu Pro Thr Ala Lys Ser Arg Thr Arg Leu Phe Gly Lys Gly Asp Ser
77 40                  45                  50                  55
79 gag gag gct ttc ccg gtg gat tgc ccc cac gag gaa ggt gag ttg gac 1325
80 Glu Glu Ala Phe Pro Val Asp Cys Pro His Glu Glu Gly Glu Leu Asp
81                  60                  65                  70
83 tcc tgc ccg acc atc aca gtc agc cct gtt atc acc atc cag agg cca 1373
84 Ser Cys Pro Thr Ile Thr Val Ser Pro Val Ile Thr Ile Gln Arg Pro
85                  75                  80                  85
87 gga gac ggc ccc acc ggt gcc agg ctg ctg tcc cag gac tct gtc gcc 1421
88 Gly Asp Gly Pro Thr Gly Ala Arg Leu Leu Ser Gln Asp Ser Val Ala
89         90                  95                  100
91 gcc agc acc gag aag acc ctc agg ctc tat gat cgc agg agt atc ttt 1469
92 Ala Ser Thr Glu Lys Thr Leu Arg Leu Tyr Asp Arg Arg Ser Ile Phe
93     105                 110                 115
95 gaa gcc gtt gct cag aat aac tgc cag gat ctg gag agc ctg ctg ctc 1517
96 Glu Ala Val Ala Gln Asn Asn Cys Gln Asp Leu Glu Ser Leu Leu Leu
97 120                 125                 130                 135
99 ttc ctg cag aag agc aag aag cac ctc aca gac aac gag ttc aaa gac 1565
100 Phe Leu Gln Lys Ser Lys Lys His Leu Thr Asp Asn Glu Phe Lys Asp
101                 140                 145                 150
103 cct gag aca ggg aag acc tgt ctg ctg aaa gcc atg ctc aac ctg cac 1613
104 Pro Glu Thr Gly Lys Thr Cys Leu Leu Lys Ala Met Leu Asn Leu His
105                 155                 160                 165
107 gac gga cag aac acc acc atc ccc ctg ctc ctg gag atc gcg cgg caa 1661
108 Asp Gly Gln Asn Thr Thr Ile Pro Leu Leu Leu Glu Ile Ala Arg Gln
109         170                 175                 180
111 acg gac agc ctg aag gag ctt gtc aac gcc agc tac acg gac agc tac 1709
112 Thr Asp Ser Leu Lys Glu Leu Val Asn Ala Ser Tyr Thr Asp Ser Tyr
113     185                 190                 195
115 tac aag ggc cag aca gca ctg cac atc gcc atc gag aga cgc aac atg 1757
116 Tyr Lys Gly Gln Thr Ala Leu His Ile Ala Ile Glu Arg Arg Asn Met
117 200                 205                 210                 215
119 gcc ctg gtg acc ctc ctg gtg gag aac gga gca gac gtc cag gct gcg 1805
120 Ala Leu Val Thr Leu Leu Val Glu Asn Gly Ala Asp Val Gln Ala Ala
121                 220                 225                 230
123 gcc cat ggg gac ttc ttt aag aaa acc aaa ggg cgg cct gga ttc tac 1853
124 Ala His Gly Asp Phe Phe Lys Lys Thr Lys Gly Arg Pro Gly Phe Tyr
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125            235              240              245
127 ttc ggt gaa ctg ccc ctg tcc ctg gcc gcg tgc acc aac cag ctg ggc   1901
128 Phe Gly Glu Leu Pro Leu Ser Leu Ala Ala Cys Thr Asn Gln Leu Gly
129         250              255              260
131 atc gtg aag ttc ctg ctg cag aac tcc tgg cag acg gcc gac atc agc   1949
132 Ile Val Lys Phe Leu Leu Gln Asn Ser Trp Gln Thr Ala Asp Ile Ser
133     265              270              275
135 gcc agg gac tcg gtg ggc aac acg gtg ctg cac gcc ctg gtg gag gtg   1997
136 Ala Arg Asp Ser Val Gly Asn Thr Val Leu His Ala Leu Val Glu Val
137 280              285              290              295
139 gcc gac aac acg gcc gac aac acg aag ttt gtg acg agc atg tac aat   2045
140 Ala Asp Asn Thr Ala Asp Asn Thr Lys Phe Val Thr Ser Met Tyr Asn
141              300              305              310
143 gag att ctg atg ctg ggg gcc aaa ctg cac ccg acg ctg aag ctg gag   2093
144 Glu Ile Leu Met Leu Gly Ala Lys Leu His Pro Thr Leu Lys Leu Glu
145              315              320              325
147 gag ctc acc aac aag aag gga atg acg ccg ctg gct ctg gca gct ggg   2141
148 Glu Leu Thr Asn Lys Lys Gly Met Thr Pro Leu Ala Leu Ala Ala Gly
149         330              335              340
151 acc ggg aag atc ggg gtc ttg gcc tat att ctc cag cgg gag atc cag   2189
152 Thr Gly Lys Ile Gly Val Leu Ala Tyr Ile Leu Gln Arg Glu Ile Gln
153     345              350              355
155 gag ccc gag tgc agg cac ctg tcc agg aag ttc acc gag tgg gcc tac   2237
156 Glu Pro Glu Cys Arg His Leu Ser Arg Lys Phe Thr Glu Trp Ala Tyr
157 360              365              370              375
159 ggg ccc gtg cac tcc tcg ctg tac gac ctg tcc tgc atc gac acc tgc   2285
160 Gly Pro Val His Ser Ser Leu Tyr Asp Leu Ser Cys Ile Asp Thr Cys
161              380              385              390
163 gag aag aac tcg gtg ctg gag gtg atc gcc tac agc agc agc gag acc   2333
164 Glu Lys Asn Ser Val Leu Glu Val Ile Ala Tyr Ser Ser Ser Glu Thr
165         395              400              405
167 cct aat cgc cac gac atg ctc ttg gtg gag ccg ctg aac cga ctc ctg   2381
168 Pro Asn Arg His Asp Met Leu Leu Val Glu Pro Leu Asn Arg Leu Leu
169         410              415              420
171 cag gac aag tgg gac aga ttc gtc aag cgc atc ttc tac ttc aac ttc   2429
172 Gln Asp Lys Trp Asp Arg Phe Val Lys Arg Ile Phe Tyr Phe Asn Phe
173     425              430              435
175 ctg gtc tac tgc ctg tac atg atc atc ttc acc atg gct gcc tac tac   2477
176 Leu Val Tyr Cys Leu Tyr Met Ile Ile Phe Thr Met Ala Ala Tyr Tyr
177 440              445              450              455
179 agg ccc gtg gat ggc ttg cct ccc ttt aag atg gaa aaa att gga gac   2525
180 Arg Pro Val Asp Gly Leu Pro Pro Phe Lys Met Glu Lys Ile Gly Asp
181              460              465              470
183 tat ttc cga gtt act gga gag atc ctg tct gtg tta gga gga gtc tac   2573
184 Tyr Phe Arg Val Thr Gly Glu Ile Leu Ser Val Leu Gly Gly Val Tyr
185         475              480              485
187 ttc ttt ttc cga ggg att cag tat ttc ctg cag agg cgg ccg tcg atg   2621
188 Phe Phe Phe Arg Gly Ile Gln Tyr Phe Leu Gln Arg Arg Pro Ser Met
189         490              495              500
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PATENT APPLICATION: US/09/587,111A   TIME: 11:05:58

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191 aag acc ctg ttt gtg gac agc tac agt gag atg ctt ttc ttt ctg cag   2669
192 Lys Thr Leu Phe Val Asp Ser Tyr Ser Glu Met Leu Phe Phe Leu Gln
193     505                 510                 515
195 tca ctg ttc atg ctg gcc acc gtg gtg ctg tac ttc agc cac ctc aag   2717
196 Ser Leu Phe Met Leu Ala Thr Val Val Leu Tyr Phe Ser His Leu Lys
197 520                 525                 530                 535
199 gag tat gtg gct tcc atg gta ttc tcc ctg gcc ttg ggc tgg acc aac   2765
200 Glu Tyr Val Ala Ser Met Val Phe Ser Leu Ala Leu Gly Trp Thr Asn
201                 540                 545                 550
203 atg ctc tac tac acc cgc ggt ttc cag cag atg ggc atc tat gcc gtc   2813
204 Met Leu Tyr Tyr Thr Arg Gly Phe Gln Gln Met Gly Ile Tyr Ala Val
205                 555                 560                 565
207 atg ata gag aag atg atc ctg aga gac ctg tgc cgt ttc atg ttt gtc   2861
208 Met Ile Glu Lys Met Ile Leu Arg Asp Leu Cys Arg Phe Met Phe Val
209             570                 575                 580
211 tac atc gtc ttc ttg ttc ggg ttt tcc aca gcg gtg gtg acg ctg att   2909
212 Tyr Ile Val Phe Leu Phe Gly Phe Ser Thr Ala Val Val Thr Leu Ile
213     585                 590                 595
215 gaa gac ggg aag aat gac tcc ctg ccg tct gag tcc acg tcg cac agg   2957
216 Glu Asp Gly Lys Asn Asp Ser Leu Pro Ser Glu Ser Thr Ser His Arg
217 600                 605                 610                 615
219 tgg cgg ggg cct gcc tgc agg ccc ccc gat agc tcc tac aac agc ctg   3005
220 Trp Arg Gly Pro Ala Cys Arg Pro Pro Asp Ser Ser Tyr Asn Ser Leu
221                 620                 625                 630
223 tac tcc acc tgc ctg gag ctg ttc aag ttc acc atc ggc atg ggc gac   3053
224 Tyr Ser Thr Cys Leu Glu Leu Phe Lys Phe Thr Ile Gly Met Gly Asp
225                 635                 640                 645
227 ctg gag ttc act gag aac tat gac ttc aag gct gtc ttc atc atc ctg   3101
228 Leu Glu Phe Thr Glu Asn Tyr Asp Phe Lys Ala Val Phe Ile Ile Leu
229             650                 655                 660
231 ctg ctg gcc tat gta att ctc acc tac atc ctc ctg ctc aac atg ctc   3149
232 Leu Leu Ala Tyr Val Ile Leu Thr Tyr Ile Leu Leu Leu Asn Met Leu
233     665                 670                 675
235 atc gcc ctc atg ggt gag act gtc aac aag atc gca cag gag agc aag   3197
236 Ile Ala Leu Met Gly Glu Thr Val Asn Lys Ile Ala Gln Glu Ser Lys
237 680                 685                 690                 695
239 aac atc tgg aag ctg cag aga gcc atc acc atc ctg gac acg gag aag   3245
240 Asn Ile Trp Lys Leu Gln Arg Ala Ile Thr Ile Leu Asp Thr Glu Lys
241                 700                 705                 710
243 agc ttc ctt aag tgc atg agg aag gcc ttc cgc tca ggc aag ctg ctg   3293
244 Ser Phe Leu Lys Cys Met Arg Lys Ala Phe Arg Ser Gly Lys Leu Leu
245             715                 720                 725
247 cag gtg ggg tac aca cct gat ggc aag gac gac tac cgg tgg tgc ttc   3341
248 Gln Val Gly Tyr Thr Pro Asp Gly Lys Asp Asp Tyr Arg Trp Cys Phe
249             730                 735                 740
251 agg gtg gac gag gtg aac tgg acc acc tgg aac acc aac gtg ggc atc   3389
252 Arg Val Asp Glu Val Asn Trp Thr Thr Trp Asn Thr Asn Val Gly Ile
253     745                 750                 755
255 atc aac gaa gac ccg ggc aac tgt gag ggc gtc aag cgc acc ctg agc   3437
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PATENT APPLICATION: US/09/587,111A   TIME: 11:05:58

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\12212004\I587111A.raw

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256 Ile Asn Glu Asp Pro Gly Asn Cys Glu Gly Val Lys Arg Thr Leu Ser
257 760             765             770             775
259 ttc tcc ctg cgg tca agc aga gtt tca ggc aga cac tgg aag aac ttt    3485
260 Phe Ser Leu Arg Ser Ser Arg Val Ser Gly Arg His Trp Lys Asn Phe
261             780             785             790
263 gcc ctg gtc ccc ctt tta aga gag gca agt gct cga gat agg cag tct    3533
264 Ala Leu Val Pro Leu Leu Arg Glu Ala Ser Ala Arg Asp Arg Gln Ser
265             795             800             805
267 gct cag ccc gag gaa gtt tat ctg cga cag ttt tca ggg tct ctg aag    3581
268 Ala Gln Pro Glu Glu Val Tyr Leu Arg Gln Phe Ser Gly Ser Leu Lys
269         810             815             820
271 cca gag gac gct gag gtc ttc aag agt cct gcc gct tcc ggg gag aag    3629
272 Pro Glu Asp Ala Glu Val Phe Lys Ser Pro Ala Ala Ser Gly Glu Lys
273     825             830             835
275 tgaggacgtc acgcagacag cactgtcaac actgggcctt aggagacccc gttgccacgg 3689
276 ggggctgctg agggaacacc agtgctctgt cagcagcctg gcctggtctg tgcctgccca 3749
277 gcatgttccc aaatctgtgc tggacaagct gtgggaagcg ttcttggaag catggggagt 3809
278 gatgtacatc caaccgtcac tgtccccaag tgaatctcct aacagacttt caggttttta 3869
279 ctcactttac taaaaaaaaa aaaaaaaggg cggccgctta                        3909
281 <210> SEQ ID NO: 2
282 <211> LENGTH: 839
283 <212> TYPE: PRT
284 <213> ORGANISM: Homo Sapiens
286 <400> SEQUENCE: 2
287 Met Lys Lys Trp Ser Ser Thr Asp Leu Gly Thr Ala Ala Asp Pro Leu
288 1             5             10             15
289 Gln Lys Asp Thr Cys Pro Asp Pro Leu Asp Gly Asp Pro Asn Ser Arg
290         20             25             30
291 Pro Pro Pro Ala Lys Pro Gln Leu Pro Thr Ala Lys Ser Arg Thr Arg
292         35             40             45
293 Leu Phe Gly Lys Gly Asp Ser Glu Glu Ala Phe Pro Val Asp Cys Pro
294     50             55             60
295 His Glu Glu Gly Glu Leu Asp Ser Cys Pro Thr Ile Thr Val Ser Pro
296 65             70             75             80
297 Val Ile Thr Ile Gln Arg Pro Gly Asp Gly Pro Thr Gly Ala Arg Leu
298             85             90             95
299 Leu Ser Gln Asp Ser Val Ala Ala Ser Thr Glu Lys Thr Leu Arg Leu
300         100             105             110
301 Tyr Asp Arg Arg Ser Ile Phe Glu Ala Val Ala Gln Asn Asn Cys Gln
302         115             120             125
303 Asp Leu Glu Ser Leu Leu Leu Phe Leu Gln Lys Ser Lys Lys His Leu
304     130             135             140
305 Thr Asp Asn Glu Phe Lys Asp Pro Glu Thr Gly Lys Thr Cys Leu Leu
306 145             150             155             160
307 Lys Ala Met Leu Asn Leu His Asp Gly Gln Asn Thr Thr Ile Pro Leu
308             165             170             175
309 Leu Leu Glu Ile Ala Arg Gln Thr Asp Ser Leu Lys Glu Leu Val Asn
310             180             185             190
311 Ala Ser Tyr Thr Asp Ser Tyr Tyr Lys Gly Gln Thr Ala Leu His Ile
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VERIFICATION SUMMARY   DATE: 12/21/2004
PATENT APPLICATION: **US/09/587,111A**   TIME: 11:05:59

Input Set : **A:\Sequence Listing.txt**
Output Set: **N:\CRF4\12212004\I587111A.raw**